OM protein - protein search, using sw model GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: June 23, 2003, 15:11:47 ; Search time 40 Seconds (without alignments) 442.218 Million cell updates/sec

Scoring table: BLOSUM62 AAK91826
965
1 MRRGPRSLRGRDAPAPTPCV.....ATELGSTELVTTKTAGPEQQ 184

Title: Perfect score:

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

al number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	. 26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	ტ	ហ	4	w	2	1	No.	Result	•
97.5	98	99	99	99	100	100	101	101	101	102	102	102.5	102.5	103	103	103	103	103.5	104.5	106	106.5	107	111	113.5	116	116.5	119	124	Score		
10.1	10.2	10.3	10.3	10.3	10.4	10.4	•	10.5	10.5	•	10.6	10.6	•	10.7	10.7	10.7	10.7	10.7	10.8	11.0		•		11.8	12.0	•	12.3	12.8	Match	Query	æ
384	1487	1487	1334	395	592	574	2240	1872	1870	365	317	862	676	3436	1952	1611	505	924	3938	325	356	2142	801	422	862	676	552	416	Length		
N	μ	44	N	N	N	N	N	N	N	N	N	N	_	N	N	N	N	N	N	N	μ	N	N	N	N	ب	N	μ.	BB		
S51796	EDBEE1	EDBEF6	T50568 ·	H75457	D70863	F75356	T37057	836152	S37671	A34894	T19143	S51493	EDBE22	855659	T48814	T38236	S72273	S27923	T42761	A55558	W JHU2H	B35098	T29018	S32357	T46289	EDBE23	T08148	SKXLAG	IB		
	immediate-early pr	155K transcription	Ç		prot	serine/threonine p	multi	class III	B III		hypothetical prote	major nitrogen reg		₼		hypothetical prote	1-dep	gene LF3 protein -			eotic protein	н			hypothetical prote	rly p	-rich	dermal gland prote			

proline-rich myrosinase-binding protein homolog - rape (fragment)
W,Alternate names: myrosinase-binding protein related protein
C;Species: Brassica napus (rape)
C;Baccies: Laway-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08148

RiTaipalensuu, J.; Falk, A.; Ek, B.; Rask, L. Eur. J. Blochem. 243, 605-611, 1997
Bur. J. Blochem. 243, 605-611, 1997
A;Title: Myrosinase-binding proteins are derived from a large wound-inducible and repeti A;Reference number: Z16379; MUID:97210758; PMID:9057822
A;Accession: T08148

RESULT 2 T08148

	45	44	43	42	41	40	39	38	37	36	S	<u>գ</u>	33	32	31	30	
	95	95	95	95.5	95.5	96	96	96	96.5	96.5	96.5	96.5	97	97.5	97.5	97.5	
	9.8	9.8	9. 8	9.9	9.9	9.9	9.9	9.9	10.0	10.0	10.0	10.0	10.1	10.1	10.1	10.1	
	2187	607	302	903	316	3164	581	548	3942	1255	708	555	353	915	896	405	
_	N	N	N	<u>د</u>	N	۳	N	N	ν.	N	N	N	N	N	N	N	_
	T30826	A43776	T32711	T00705	T19291	WMBEH6	T22341	S52735	T42730	T31065	D96711	T30349	S36249	S36327	S36326	G70829	_
	nascent polypeptid	drebrin E2 - chick	hypothetical prote	N-chimerin homolog	hypothetical prote	UL36 protein - hum	hypothetical prote	CW17R protein - mo	Bassoon protein -	diaphanous protein	hypothetical prote	. structural protein	lipB protein - Pse	clathrin assembly	clathrin assembly	probable molybdenu	

ALIGNMENTS

Qy 12 DAPAPTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVG 64
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C;Species: DOVING C. (Species: DOVING C) Date: 31-Dec.1992 #Bequence_review.
C;Caccession: B38209
R;Witth, U.V.; Fraefel, C.; Vogt, B.; Vlcek, C.; Paces, V.; Schwyzer, m.
J. Virol. 66, 2763-2772, 1992
A;Title: Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 A;Reference number: A38209; MUID:92219360; PMID:1313901
A;Accession: B38209
A;Accession: B38209
A;Accession: B38209
A;Accession: B38209
A;Accession: B38209
A;Accession: B38209
                                                                                                                          RESULT 4
T46289
                   hypothetical protein DKFZp434Al010.1 - human (fragment)
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
(;Accession: T46289

,R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
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C;Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
C;Keywords: DNA binding; immediate-early protein; transcription regulation; zinc finger
F;9-57/Domain: RING finger homology <RNG>
F;13-51/Region: zinc finger C3HC4 motif
F;284-331/Region: acidic
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A;Molecule type: mRNA
A;Residues: 1-552 <TA
A;Cross-references: E
    submitted
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Matches 62
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                                                                                                                                                                                                                                                 158 GHSVPVPATELGSTELVTTKTAGP 181
                                                                                                                                                                                                                                                                                            461
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                                                                                                                                                                                                                                                                                                                                                                            406 AAQARACSPEPR-----EEGRGAGLGVAAGETAGWGAGSEEGRGERRARLLGEAGPPRVQ 460
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                                                                                                                                                                                                          GAQIGTPA----AAAAVTAAAAAP
                                                                                                                                                                                                                                                                                            ARRRRTELDRAPTPAPAP----APAPAPISTVIDLT----ANAPARPADPAPAAAPGPASA
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A.; Lauber, J.; Mewes, H.W.
e Protein Sequence Database,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 116.5; DI Pred. No. 0.27;
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Pred. No. 0.15;
7; Mismatches
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  January
Gassenhuber,
January 2000
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  RESULT
T29018
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RESULT 5
S32357
glial growth factor - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_re
C;Accession: S32357
C;Taccession: S32357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: Z23035
A;Accession: T46289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-862 <AAA>
A;Cross-references: EMBL:AL137579
A;Experimental source: adult testis
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Glial growth factors are alternatively spliced A;Reference number: S32357; MUID:93205115; PMID:8096067 A;Accession: S32357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; Hen les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M. Nature 362, 312-318, 1993
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A; Residues: 1-422 < MAR>
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 140 VPSWPTAPVPS
                                                                                                           107
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                                                                       GALDRKAAAAGEAGAWGGDREPP
                                                                                                         ----RLRGASSAEAP--DGDKDAPEPLDKVIILSPGISDATAP-AWPPPGEDP-----GT
                                                                                                                                           LGTAALAP---
                                                                                                                                                                               APRTALQPQESVGAGAGEAALPL-PGLLFGAPALLG----LALVLALVLVGLVSWRRRQR
                                                                                                                                                                                                                                                       RRGPRSLRGRDAPAPTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSP------
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                                   TPPGHSVPVPA 165
                                                                                                                                                                                                                     RRAPRR-SGRPGP-----
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150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17,
                                                                                                                                                                                                                                                                                       Score 113.5; DI
Pred. No. 0.29;
5; Mismatches
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Pred. No. 0
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                                                                     - AAGPRALGPPAEEPLLAANGT
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                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                   106
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                                                                       139
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R;Banerji, J.; Sands, J.; Strominger, J.L.; Spies, T. Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990
A;Title: A gene pair from the human major histocompatibility complex encodes large prol A;Reference number: A35098; MUID:90192810; PMID:2158268

AAccession: B35098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Nolecule type: DNA
A; Molecule type: Cone type: A; Residues: 1-801 < KIR>
A; Cross-references: EMBL: U23181; PIDN: AAC48204.1; GSPDB: GN00020; CESP: ZK84.1
A; Cross-references: STRAIN Bristol N2; Clone ZK84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kirsten, J.

R;Kirsten, J.

submitted to the EMBL Data Library, April
A;Description: The sequence of C. elegans
A:Peference number: Z20553
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C;Accession: B35098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T29018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ZK84.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #
                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-2142 <BAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2
A; Introns: 22/2; 45/3; 108/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T29018
                                                                                                                                                                                                                                                                                                                                            ;Cross-references: GB:M33509; NID:g179338; PIDN:AAA35585.1; PID:g179339; NOte: the authors translated the codon AGT for residue 97 as Gly;Superfamily: collagen alpha 1(IV) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        class III histocompatibility antigen HLA-B-associated protein 2 [imported]
                                                                                                                                                                                                                                                                                           Local Similarity
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    PEQQ 184
                                                                          DAPEPLDKVIILSPGISDATAPAWPPPGEDPGTTPPGHSVPVPATELGSTELVTTKTAG- 180
                                                                                                                    TPGVA-AAPTLVS-
                                                                                                                                                     LPGLLFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDG------DK
                                                                                                                                                                                             PAPPPAVPKE---
                                                                                                                                                                                                                               PAPTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VII-----LSPGISDATAPAWPPPGEDPGTTPPGHSVPVPATELGSTELVTTKTAGP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPLPGLLFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAP-EPLDK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAPAPTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTA-LQPQESVGAGAGEA
                                          EGPEPPEEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                         11.1%; Score 107;
25.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 111; DB 2; 25.4%; Pred. No. 0.81;
                                                                                                                                                                                                                                                                       16;
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                                      TTPPVPKVEPKGDGIGPTRQPPSQGLGY 624
                                                                                                                -GGGSTSSTSSGSFEASPVEPQLPSK 584
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                                                                                                                                                                                                                                                                                                          Length 2142;
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A; Residues: 1-42 < VI2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate
                                                                                                                                                                                                                                                                       F;144-200/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:HOXB2
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Best Local
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R;Giampaolo, A.; Acampora, D.; Zappavigna, V.; Pannese, M.; Differentiation 40, 191-197, 1989
A;Title: Differential expression of human HOX-2 genes along A;Reference number: A37042; MUID:89378558; PMID:2570724
A;Accession: E37042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: homeotic protein Hox B2; homeobox homology C:Kevwords: DNA binding; homeobox; nucleus; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:120665;
A; Map position: 17q21.3-17q21.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 132-135,'RRL',139-208 <GIA>
A;Cross-references: GB:X16176; NID:g32378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Vieille-Grosjean, I.; Huber, P.
J. Biol. Chem. 270, 4544-4550, 1995
A;Title: Transcription factor GATA-1 regulates human HOXB2 gene expression A;Reference number: A56093; MUID:95181447; PMID:7876223
A;Accession: A56093
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A;Residues: 143-202 <KON>
A;Residues: 143-202 <KON>
A;Cross-references: EMBL:X14571; NID:g32034; PIDN:CAA32709.1; PID:g930065
A;Cross-references: EMBL:X14571; NID:g32034; PIDN:CAA32709.1; PID:g930065
A;Cross-references: EMBL:X14571; NID:g32034; PIDN:CAA32709.1; PID:g930065
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                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: DNA binding; home F; 76-96/Region: proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X78978; NID:g475199; PIDN:CAA55581.1; PID:g475200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 143-208 <BON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X16665; NID:g32381; PIDN:CAA34655.1; R;Kongsuwan, K.; Webb, E.; Housiaux, P.; Adams, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S07541; MUID: 90098876; PMID: 2574852
A;Accession: S07542
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                                                                                                                                                                                                                                                                                                                                  Local Similarity
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APALLGIALVLALVLVGLVSW--RRRQRRLRGASSAEAPDGDKDAPEPLDKVI-----I 132
                                                                                SÁTSPSPAASAVPASGVGSPADGLGLPEAGGGGARRIRTAYTNTQLLELEKEFHFNKYLC 169
                                                                                                                                       GASSPAPRTALQPQESVGAGAGEAALPLPG--
                                                                                                                                                                                           PRS-LRGRDAPA----PTPCVPAECFDLLVRHCVACGLLRTPRP----
                                                                                                                                                                                                                                                                                                   11.0%;
ilarity 24.7%;
Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                     Score 106.5; DI
Pred. No. 0.81;
6; Mismatches
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E.

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Bassoon protein - rat
N;Alternate names: brain-specific synapse-associated protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42761
                                                                                                                                                                                                                                                                                                     RESULT
T42761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiene (man)
C;Date: 18-Aug-1955 #sequence revision 18-Aug-1955 #text_change
C;Accession: A55558; G02887
R;Khatib, Z.A.; Inaba, T.; Valentine, M.; Look, A.T.
Genomics 23, 344-351, 1994
A;Title: Chromosomal localization and cDNA cloning of the human
A;Reference number: A55558; MUID:95137580; PMID:7835883
A;Accession: A55558
                        A; Molecule type: mRNA
A; Residues: 1-3938 < DIE>
                                                                                    A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat A;Reference number: Z22249; MUID:98345363; PMID:9679147 A;Accession: T42761
                                                                                                                                                R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, J. Cell Biol. 142, 499-509, 1998
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(Cross-references: GB:U06936; NID:g606798; PIDN:AAA81374.1; PID:g606799
R;Mueller, C.R.
Submitted to the EMBL Data Library, February 1996
A;Reference number: H01797
A;Accession: G02887
    A; Cross-references:
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A; Residues: 1-178, 'S', 180-325 < MUE>
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Matches 55
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rons: 47/1; 184/1; 254/3
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EMBL: Y16563; NID: g3413503; PIDN: CAA76287.1; PID: g3413504
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Pred. No. 0.81;
                                                                from GB/EMBL/DDBJ
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                                                                                                                            selectively localized
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RESULT
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A,Description: may be involved in cytomatrix organization at the site A;Note: component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
actin-depolymerizing protein N-WASP, brain - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 23-Apr-1998 #sequence_revision 01-May-1998 #C;Accession: S72273 C;Accession: S72273 R;Miki, H.; Miura, K.; Takenawa, T. EMBO J. 15, 5326-5335, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene LP3 protein - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
C;Accession: S27923
R;Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell
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C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
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A; Residues: 1-924 < PAR>
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Pred. No. 11;
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of Raji Epstein-Barr virus DNA
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RESULT
T48814
                   R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24541 A;Accession: T48814
                                                                                C;Accession:
R;Schulte, U.
                                                                                                 hypothetical protein 15E6.220 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change C;Accession: T48814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 03-Dec:1999 C;Accession: T38236
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A; Residues: 1-505 < MIK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: D67066; NID: g1644231; PIDN: BAA11082.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
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                                                                                                                                                                                                                                                                                                              PLDKVIILSPGI---SDATAPAWPPPGEDPGTTPPGHSVPVPATELGSTELVTTKTAGP 181
                                                                                                                                                                                                                                                                                                                                                                                               PLPGLL-----FGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APAPTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QESVGAGAGEAALPLPGLLFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPARGRGAPPPPPSRAPTAA--------PPPPPPPSRPGVGAPPPPPNRMYPP
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                                                                                                                                                                                                                                                                       PVPKPSVAAPPVPAPSSGIPPVPKPAAGVPPVPPPSEAPPVPKPSVGVPPVPPPSTAPP
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Pred. No. 2;
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A;Cross-references: GB.UZ0824; NID:g695172; PIDN:AAC13852.1; PID:g695237 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Febru.
                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, 71915
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A;Map position: 2
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Best Local :
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                                                                                                                                                                                                                                                                                                     Similarity
KKQQGAAEAEAPA-PREGEGAAQEAPGEGTPEPAS-IGKT 3345
                                                                                                       LVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPLDKVIILSP-
                                                                                                                                                                           G-----LLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGLLFGAPALLGLA
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                                 -GISDATAPAWPPPGEDPGTTPPGHSVPVPATELGST 171
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                                                                                                                                                                                                                                                                                                     10.7%; | Score 103; 25.0%; | Pred. No. :
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Pred. No. 7
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                                                                    - PE-TOTADY IEPPKSGVGAGSGPPE
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